

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gatanaga, T.
Granger, G.A.
- (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity
- (iii) NUMBER OF SEQUENCES: 154
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 09/081,385
(B) FILING DATE: 014-NOV-1998
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTTC	CTTTCCTTCC	CCGGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCCGCGCG	180
TGGGGCCCGG	CGGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCCG	240
TGCGGGCGCC	AGCGCCGTGG	GTGGAGGTCG	CCGTCCCTCC	TGAGGGGCAG	CCAGTGCGTT	300
TGGGACCCGG	GAGCAGAGCC	CGCGCTCCC	CAGCGGCCTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGCCCCG	GCTCCGACAG	AACCCGGGGG	GGCCCGGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
TGGGTTCGGT	GCGGGACGGC	CCAGGCCGCC	AGGACCCCA	AGCGCAGCTC	AGTCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGAGGTTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720

AGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AGGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TGCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTCAAG	900
ATTTTCAGGA	GTTTCAGGTG	GAGACAAAGG	CCAGGCCAG	GTGAAATGT	GGCAGTGACA	960
GAGTATGGGG	TGAGAACAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
CGGGGACCAG	AATTTTTTAA	AACGCATCTG	AGATGCGTTT	GGCAGACTCA	TAGTTGTTTT	1080
CCTTTCACGG	AGAAAGTGTG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCTC	CCTGTACACG	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAAGCTG	ATCCGCCCCG	ACCCAGGGCC	1260
CCCCGGGTGC	CCCTTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAACA	1320
CCGGACACGG	GTCGTGTGCT	GCACCTGGCA	GTTGCAGGAC	CGACACCCAC	AATGCCTTAA	1380
GAGGTGATGA	CTGCCTTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
GAGGGATTGA	GTGGAGTCCA	CGGGTCATGG	CCACGCTCTG	GGTGTCTCCT	CTGAGGCAGG	1500
GCCCGGCTGG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTCTG	CAGTTCAGCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAACC	CACTGGGGGG	TTATGAAACT	GCAGGTGGCT	GAGTCTTTC	1620
CATGGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGTACCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGATGTGGC	CTGGCGTGTG	GTGGCTCTGG	ACCTAGTCTT	TGGGCTTGGG	1740
CTGGCGCCCA	GGGCTTGGGC	TTGAGACAGC	TGTACGCAG	GCAAGCCATT	TACCCCGTTT	1800
GTGGGGACAT	TACATCTTCC	TAGCTTGGAA	CACACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
TCCTCCTCCA	TGTTCTTCTC	TTGAGAACTT	TTACCAGGTA	TGTCAGGAGC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGAAA	GCCCTCATCC	TTGTCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GCGATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTTCT	CCACAGGAGG	2100
AAGCGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGGAACA	GTGCGCGCAG	2160
AACCAACAAC	CACCCCCACC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCCTGCT	GGATCTTAGG	TCTTGTCTT	GGGCAGCTCT	GCTGAGACCT	2280
CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTACTATT	GGTCTGGGGT	TGTTTTGCAG	2340
CAACTGAAGT	GTTCTGTGTG	AAAACAGGCA	CTTGATTTC	TGGAAGGAAT	GCTGTTTGT	2400
CTTGCTGCGA	CAAACATTGA	GCAGCATTTA	GTGGGCGGTT	TATATCTTGT	GGAGTAATGG	2460
GTGTTTTTGA	AGTCTGTCTT	GGGTACTGCA	CATTAAAAGG	AATATCATTT	TCTGAAACAT	2520
TGCTATTTTC	CACACCAGAA	ATCATATCCT	CTTGCTGGTC	CATGTCTGAA	GACCTTACAC	2580
GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAACTAATT	ATATCATACA	2640
TTGCCGCTTT	CTCACTCTGC	TCTTTTTTCT	CCTTGCCTAA	TTTCATTTTC	TTCTGCTTCT	2700
TTTGTTTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTGG	AACATCTCGA	GGTGATGAAC	2760
AAGGTAGAGA	CTGAGATTGT	AGGATTAAAG	GTGGTCTTGA	GCCTTTAGGA	GTTCCCTTCA	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCTCTA	2880
TTGTTGAAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGCAC	CATGTGTAGG	TAGTCTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAG	3000
AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
CTTGTTGCAT	CTGTGGATGT	GTTGTGTAAC	TTGAAGGATG	GGAATATGGC	ATGTATCCTG	3120
CAGGGCTTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAATCTGT	3180
TCCCAGAGCT	TGTCGTGGT	GGCACAACCC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTTT	3240
GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360
GACTCCTTGC	CAGGACGGCC	TGCAACAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
CAAGGTTATC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTTGAGGCTA	TGGACAAGCT	3480
GTGAAACCAA	ATTGTCACTC	CTACAAGCCA	AAAGGCAGTT	CACCTCTTCT	GCTATTCTGT	3540
CATTAAAGAG	AAGGCTCTTT	GTAGTTGTAG	CAGGTAAAGG	AGATGGAAGA	GGCAGCTGGT	3600
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
CCCCATTTCAT	CCTGAATTTC	TGGAATGGTG	TTGCCTATAA	AAGTACTTAG	TTCAGGTGCC	3720
AGCTGTCATT	ACTTCCCAT	TCCCAACAC	TGGGCGAATC	GGCGTCTGAA	TCCAAGGGGA	3780
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
CCTCTCCGT	CTCCTCAGTG	CGGGGAACAT	GTAGAGCCGG	GGGGAGACCA	GCCGAGAAGA	3900
CAAAATCGTTG	CTTCTTCTTC	CTCCTCCTCC	TCCTTCTCCC	ACATAGAAAC	ACTCACAAC	3960
ACCCGACCAC	GGGCCCGAGC	TACCGGGGGG	GCATCGCCCG	GGGCCCGGGA	ACCAATTCTC	4020
CTGTCGGCGG	GGGCGTCTTT	TGGATCC				4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAAG	GTCAAACCTCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCCG	GCCCGGCCGG	60
CGCGCGGCCG	GGCGCTTGGC	GCCAGAAGCG	AGAGCCCTC	GGGGCTCGCC	CCCCCGCCTC	120
ACCGGGTCAG	TGAAAAACG	ATCAGAGTAG	TGGTATTTC	CCGGCGGCC	GCAGGGCCGG	180
CGGACCCCGC	CCCGGGCCCC	TCGCGGGGAC	ACCGGGGGG	CGCGGGGGC	CTCCCACTTA	240

TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC 300
 TTTCCCGCT GATTCCGCCA AGCCCGTTCC CTGGGCTGTG GTTCGCTGG ATAGTAGGTA 360
 GGGACAGTGG GAATCTCGTT CATCCATTCA TGGCGTCCAC TAATTAGATG ACGAGGCATT 420
 TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTTAC CCGCGCTTCA TTGAATTTCT 480
 TCACCTTGAC ATTCAGAGCA CTGGGCAGAA ATCAGATCGC GTCAACACCC GCCGCGGGCC 540
 TTCGCGATGC TTTGTTTTAA TTAACAGTC GGATTCCCTT GGTCCGCACC AGTTCTAAGT 600
 CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCC CGGGGCGGAC 660
 CCGCGGGGGG GACCGGGCCG CGGCCCTTCC GCCGCTGCC GCCCGCGCCG CCGCCGCGGC 720
 CCGAAGAAGA AGGGGGAAA 739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC GGCCGCAGCA GGCCCCCGG GTGCCCGGGC CCCCCTCGAG GGGGACAGTG 60
 CCCCAGCCGC GGGGGCCCCG CGGCGGGCCG CCGCGGGCCC CTGCCGCCCC GACCTTCTC 120
 CCCCAGCCGC CGCCCCACG CGGCGCTCCC CCGGGGAGGG GGGAGGACGG GGAGCGGGGG 180
 AGAGAGAGAG AGAGAGAGGG CGCGGGGTGG CTCGTGCCGA ATTCAAAAAG CTT 233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG AATTCGGCAC GAGGTAGTCA CGGCTCTTGT CATTGTTGTA CTTGACGTTG 60
 AGGCTGGTGA GCTTGGAAAA GTCGATGCCG AGCGTGCAGC AGGCGTTGTA GATGTTCTGC 120
 CCGTCCAGCG ACAGCTTGGC GTGCTGGGCG CTCACGGGGT CCGCATACTG CAGCAGGGCC 180
 TGGAACTGGT TGTCTTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGAA CTTGGAGAAA 240
 ATCTGGTGCA GCACATCCAG GGTACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC 300
 ACGGGGCTCT GCCCGGCCAT CGCCATCCCT GCATCCACGG CCGCCGCCGA GGCAGCCAAG 360
 GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CCGCCTGGGC CCGCGCCTGG 420
 TTGGGAGAGC TGTGGTCTT CAGCTCCTTG TGGTTGGAGA ACTGGATGTA GATGGGCTGG 480
 CCGCGCAGCA CAGGGGTCAC CGAGGTGTAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC 540
 GTGTTTCTCT CGATGAAGGC CTGGTTTTTC CCCTTCAGCA TCAGGAGGTT GGTGACCTTC 600
 CCAAAGGGCA GCCCAGGGA GATGACTTCC CCCTCCGTGA CGTCGATGGG GAGCTTCCGG 660
 ATGTGGATCA CTCTAGAGGG GACGCTGCA CTTGCGGTGT CACCTTTGAA CTTCTTGCTG 720
 TCATTTCCGT TTGCTGCAGA AGCCGAGTTG CTGCTCATGA TAAACGGTCC GTTAGTGACA 780
 CAAGTAGAGA AAAGCTCGTC AGATCCCCCG TTTGTACCAA CGGCTATATC TGGGACAATG 840
 CCGTCCATGG CACACAGAGC AGACCCGCGG GGGACGGAGT GGAGGCGCCG GAATCCTGGA 900
 GCTAGAGCTG CAGATTGAGT TGCTGCCGTA GACGAAGCGC AAGTATGAGA GTGTCCTGCA 960
 GCTGGGCGCG GCACTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG 1020
 TGATGCCCTT GCTGACCTCA GCCAGAAGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA 1080
 TGCAGAGACA CAGAACTAC TATGCAAGAA TGGGGAACG CTGCTAGGAG CCGTGAACCT 1140
 CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG GAAGACACGC TCATGACTGT 1200
 GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT 1260
 GAGTCTAGGC CCCCAGGATG CAGGGACACG TGGTCGACTT GAGAGTGCCC AGGCCACTTT 1320
 CCAGGCCCAT CGGGACAAGT ATGAGAAAGT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT 1380
 CCTGGAAGAA AACAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT 1440
 GTCCGCTTAC TTTGCTGGGA ACCAGAAACA GCTGGAGCAG ACCCTGCAGC AGTTCAACAT 1500
 CAAGCTGCGG CCTCCAGGAG CTGAGAAACC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC 1560
 CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAAGGCA GCCCAGGGT GTGGGAGATT 1620
 GGACATGGTA CATCTTTGT CACTTGCCCT CTGGCTTGGG CTCCTTTTTT TGGCTGGGGC 1680
 CTGACACGAG TTTTGCCCA ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAGTTG 1740
 CTGCCCTGTC TATCTTCTG GCCACAGGGC TTCATTCCCA GATCTTTTCC TTCACTTCA 1800
 CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCCAATGG ATCACTCTTC AGGCTGGGGT 1860
 GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTTCTC 1920
 GGACTCCCTT GGGCCAATGA TGTTCGCTCT AATACCTTT GTCTCTCTC TATGCGTGCC 1980
 CATTGCAGAG AAGGGGACTG GGACCAAGG GGTGGGGATA ATGGGAGGCC CCATTGCTGG 2040

CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATCTACT AATACATTTT ATTTGTGTTT 2100
TCTAATTTAA AATTACCTTT TCATCTTGCT TGATTTTCCT TCAGCTAAAT TAGAAATTTG 2160
TAGTTTTTCC CTTAAAAAAT TCAATGGCAT TCTTTCTTAT AAATTACATT CTCTGATTTT 2220
CTTGTGAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTGCTCGCA GTTTGCTCCA 2280
TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTCTGGAGA 2340
AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC 2400
TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATACTGGA TATGCAGTGT TCCAGACAT 2460
CACTGGTCCC AAACCATTTT TTCTGCCTGC CACTGCCACA AATACAGTAG GAATGCCATC 2520
CCCTTCATAC TCAGCTTTAA TCCTCAGAGT TTCATCTGGT CCTTTATGCG CAGATGTTAC 2580
TCGAAGTTCA CATGGAATGC CAAAATTTCC ACAGGCCTTC TTGATTTTTT CACAGTGACC 2640
AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCTGCGAC TGACTTTCTG ATTTCAAAAG 2700
CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTTT ACCATTGGA GCCCTTCAGG 2760
AGTTACTTCT TTGAGTCCC GATAAGACTG TTTGTCTTTC TGTGGCTTC GATCTCCTGA 2820
TGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT 2880
TACATCAACA CCAAATTCAT TCTTCATATC AACCACTGTA CAATTCTGGG GCAACCAGGA 2940
TTTCTCCAGT ATTTCAAATA TAGCCTGTGT AGCATCTCGT GCCGAATTC AAAAGCTT 2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTTG TGAACCCCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC 60
CTGCCCCAGG ACATGACGAT GCCTCACACA CACACACACA CACACATACA CACAAGGCGG 120
TGAGCTGCAC GCAGGAACAT GGGCTGCACT CACGACAACA TTGAAAAAAT ATACATTATA 180
TATGTACACC CGGGGCCCCC ACGTCCCCCT CCGTCCCCGC AGCCTGGCCA CACCAGGTCA 240
CGGAGGAGGG GCCGGGGCTG CAGGACCTCA GGAAGGAGG GGCAGGAAGG GAAACAGGAC 300
AAGAAAGGAA GGAAGTTGGA AAGGAGGGAG AAATGGGGTC CCCAGACTGA AATGGAAATG 360
AGGTGGGGCG ATCATAAGAG AAGCAGGGAC GATGTTCCAG CTGAGGGAGC CCTGCAGAGG 420
GGGAAAGCT TCCATGGAC AGGAGAGAGA AGGGAAGGGG AGAGGAGAGG GTTTCTCTCA 480
ATCCACCCCC CAGCCCCAGC CCCAGCCCCA GCCATTGCAA TCGTCACCTT CTCCCAACA 540
CAGTGAGTGC TAAGGGGGCA GCTGCCATTG GGGGTAGAAA GGCAGCTGAA GTCCAGCCCA 600
CTTTCCAACC CAGCCAGCCC CAGTGAAGG GGCACACCAG GAGCATGACA GCCCAGAAAT 660
GAGGGATGGG GGGCCGGGGG AGGGGCAGGG CGGACTCCAG AGGGCCCGCT GGGGTTTTGA 720
AATGAAAGGA GGAAGTCTT TGAAGCCTCT CTCCCTCTTG GTCTCTGTGT TCCCAGAAAG 780
TCCTTCTCCC ATGTCTGGAG TGTCTGTTTC ACCAGGGCAG AATTCCTCTT CTGCGTGGGG 840
AGAGGTGTAG GCCTTAGTAG CGGTGTGGGG GGGTCTCGAT GATGCGTCTC TCGTCTGCTG 900
TGCGGGGAATC GGCCACCTCC GAGTCACTGC TGTCTCTATC CTCTGCTGG CCCCCAACAG 960
CCCCCGTCAC ACAGGACTGC CGATTCTGGT AGGACTCCAT GGGGTTTACA ATGATGGTGA 1020
GAGCTGAGTC ATCCAGAAAG AGGTCTGGGT CCTTGGGGTC ACTGGAGGCC CCTGGAGGCC 1080
CGCCGGCCCC TGAGACGCGG CGGTGAAGGG AATGGATGCG CACCAGGCCC AGGACGACCA 1140
TGAGCACCCAG GAAGCCACAG CACACCACAA TGATGAGGGT TGCAGGCGTG GGTATCATGG 1200
AGTTTCTGTG GGAGCTGGCT AGGCTGTGTC CAGCCATCTC AGGCGGGGGG TGGTGACCAC 1260
GGTGCAGGAA CTGCTGGGAG CTGAGCACGT GGCTGGGGTG GGCAACCCGG TTCTGCTGT 1320
GCAGGACATT GACCTCCACG ATGAATTCAT TGCTGGAGTA ACGGCCATTC ATTTCCGAGC 1380
AGGAAAGCCG GAATCTCTG GTGTAGAGGG CAGTCCGTG TCGCAGCCGA TAACGAGCCT 1440
GCCTCAGGAT CTCTTCATAC ACAGTGATGC TCTCCACCCC AGCAATAGTG AGGTAGGCAG 1500
ATGTGTTGGT GAGCTCCAGC CCCCCTGTCT GCAGAGAGGT TGTGTCCAGG AGCAGGCTTT 1560
CCCGCTCGGG ATCCAGGTCA TCCCCACCA GAGAAATTTT ACAGCCATCC AGGTTGTGCA 1620
CAATCTCATC CGACATGCGT GTGTCTGTCA CTGTGCCCTG CCAACTCTCA TCCTTTTTGG 1680
CCTCCACCTG GTGAGAAATG GAGCAGGTGA TTTGAAGATC AGGGAACAAA GGGACGCCGT 1740
TGGTTCCCTC AAAGTCCACA GCTGGGGCGG CAAAATGAGC AGTGCCACTC AGCAGGATCT 1800
GGGGGGCGTC AGGTGAAAGG ACGACCACGT AGCCCTCCAC TTCAGGGATG GAGACGCAAG 1860
ACTCTTCTGT GAAGCACTTG ACAGCAGTGG TGAGGCGCAG GGGCCTGACG CCGGGCGTGG 1920
CAAAGCGCAG AGTGTTCATG TAAGCCACAT GCTGCAGGGC ATGGTTGAAG GTCTCCACAT 1980
CATCCCCCTC CAGGGTGAGC AGGACTGTG AGGGGTTTAC GTGGACCTTC ATGCCCTTGC 2040
CCAGGCTCTC GAAATCCCTA TAGTCCAGCC CCTCCCGACA TGCATAGAGG CACTCGATGA 2100
CCTCGCGGCT CTCCAGGCCA CTTGAGCGCA CGCTGAAACC AGCCAGGTAG CCATGGAAGT 2160
AGTGGTGGAT CGACAAAGGG TCTCTTGGG TGGTGTCTGT ACTGTTGTCT CCCTTTCTCT 2220
TCTCTTGTG CTTCTCTCA GTCCAGCAGG CCCCATCAT GAGAGCAGGC TCCCTTCGGG 2280
GTGGGTGGAT GAGGCCATTG TCATGGATGA GGGCAGGGTC GAAGGAGATG CCGTCGGTAT 2340
AGAGTGTGAC TGTGGGGAAC TCGAGGTTCA GAGCGTAGTG GTGCCACTCA TCATCACAGA 2400
CCTGCTCCAG CTTCAGAGG AACTTGACTG GCGGGGCACT CTCAAGCAGG GGCCAGTAGA 2460
GGAAGGCAAT CCTACAGCCG TGGACAGTCA GCGAGTAGTG AGAGAAGCCG TCCTCATTCT 2520
GGACAGTGT ACATACGATG GTTCTCTCT CTTCTTGGC CTTGTTGGGA GTTACGCCAT 2580
GCTTCAATCA GAAGGACAGG GTGAAGTGGT CACTGAGGCT GTCTGGGGC CCAGAGCCCA 2640

GCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTGTGTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	GAGTTTCCGC	AGCGCCCGCT	2820
CTGAGTAGTT	GTACCGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCACG	ACCTGGTGCA	TATTCGATCC	TTTTGTCCA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCGCTTC	TTCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGCC	TCTCACCCT	GACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCCTCATTG	TCAATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCTCT	GTACACAGCG	CACGATACAG	CCGTTCCACA	AACACTGGGG	3300
CAAACCTCGT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCCTGGAT	GGTGAAGGTG	TGTTCTTCT	3420
GGGCTCGCA	GTCCACAGGC	TCCTTGGCCC	GGATCAGCCC	CTCTCCTGTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAGGGC	ACCCAGAGCC	CATGGAGCCG	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCAATCTC	CATGACGATG	CCCTGGTACT	CTGCCCTCAAT	CCATGGCTTG	TGCTTGTGG	3660
CTTTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGCG	GCGTGGGGCA	GGGCAGGGCC	AGGCCTTTGC	CTCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTC	CACCTTCCGG	GAGGGATACA	GGGGGGGAAA	ACCAAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCTCTGCG	AGGTTACAGG	GATCACTGCT	GCCACCACCG	CCACCCTGGG	AGCCAGTTAT	3960
TTTGCCATGG	CCTTGATTGC	AACAGCTGCC	TCCTCTGTCA	TGGCAGACAG	CACCGTGATC	4020
AGGATCTCTT	CTCCACAGTC	GTACTTCTGC	TCAATCTCCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCGGCAGC	AGTGGCCACA	TCATGAACCT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAGCG	GAAGCGTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCTTGCA	GCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCAGC	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTGTGT	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTCAAC	ATGGAAGTGC	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCGC	480
ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCCTGA	GGAAGTGAAG	CGGGAGAAAG	540
CGGGGGGGCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGCA	CCCTGAATT	CTTCCACGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTGCGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCCTCGCA	GCAACCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGCAA	GGCCCTTCTG	CAGGACTCAG	1020
CCCCGCAGCC	AGCGCTACCT	CAGGTCCAGA	TCCCCTTCCC	CCGCGGCTCC	CGCCGCCTCT	1080
CTAAGGAGGG	TATCCTGCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTTT	CTACATCACT	GGCCCTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCTGAA	GCTCTGGGAT	TCCCGCTGGA	GCTGAGGGAG	TGCGAGCTAC	1260
TGCCTGATGG	GGAGAGACTA	GCACCCAATG	GCCGGGAGCG	AGAGGCTCCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGCGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCAGGA	GGCCAATTGG	CTGACCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGCAAA	GGATGGCAGT	GGTTCTGAAG	1500
AGAAGCGGAA	AAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGCCTGT	GCGAACTGTG	GACCCAACTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCCTGCTG	AGCACAAGCC	ATCAGTCATC	GTCAACCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCCAGGCCC	GAGCCCTCA	1860
TCATCCCCAC	CAAGCGGGGC	ACTTTCATCG	CCCCTCCCGT	CTACTCCAAC	ATCACCCCAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCGG	CCCCCATCC	TCAGCCCTGT	GCGGGAAGGC	TCTGGCCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCCCC	TCCTCCCATC	ACGCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAACA	GTGCTGAAGT	AACCCCGCCT	GTCTCTCTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGGC	TCCCGGTTCC	2220
AGGCAGAAAT	CCCCTTGATG	AGGGACCGTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGTCTGCAC	GAATCCAGAG	GAGACATCCT	GGAACCGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCCTGCGG	CCCCACAACC	ATCCGCTGGC	AACTTATCAC	TACACAGGCT	2520
CTGACCAAGT	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAGA	2580
AGGATTTCTT	CCTGGTGAG	AAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCCAAAAGTT	CCCAAGGGTG	CCTCTTCCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGCCCAGGA	AGGAGGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCAG	GCGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAGTGCACG	AAGGGCACTA	CCTTTTTTCT	AAAAAAAAAA	AAAAAAAAAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGTCAGT	TTCTGTGGA	ACACAGAGGC	TGCTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATA	GGGATCCCAA	CAGTGGATTT	GTGTTTAATC	120
TTAATCCGCT	AAACAGTTTC	CAAGGATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTATGT	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACCATCCT	GGGAAAACCT	GCTTCTGGCT	240
GTGAGGCAGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGAA	GCCAGCAAGG	CCAGTCGGAA	300
TTGAGAAAAG	CCCTCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGET	GATGCTTTTA	TCGTCCGCTT	TGTTTGCAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATTC	CTGCATCAAG	ATATCGACTC	TGGGCAAGGG	ATCCGAAACA	480
CTTACTTTGA	GTITGAAACC	GCGTIGGCCT	GTGTTCTTTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGGA	600
CGGCTGTTGA	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTGAGC	GTITGCAATC	660
CTCTCCCTTA	CATTCTGGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTGAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGACAG	TGAGTCCCA	AGCCGCGGCG	AATGGATCTT	780
TGAGCATCAT	GTATGTCAAC	GGTGACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCGGGCTCAC	CAGCATTTCA	GCTTCAGGAT	GGTTGTGAGT	900
ACGTGTTTAT	CTGGAGAACT	GTGGAAAGCT	GTCCCGTTGT	CAGAGTGGAA	GGGGACAACCT	960
GTGAGGTGAA	AGACCCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCTTG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTTCCT	1080
CAGACGCTCT	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTGAG	GAAGAGCGGG	1140
AACCGCAGGG	ATTTACAAAA	GTGGCAGGTC	TCCTGACTCA	GAAGCTAAGT	TATGAAAAATG	1200
GCTTGTAAAA	AATGAACCTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTCTTA	AAGGAGACTT	1320
CAGATTGTTT	CTACTTGTTT	GAGTGGCGAA	CGCAGTATGC	CTGCCACCTT	TTGATCTGA	1380
CTGAATGTTT	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTCC	CTGTCAAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGGA	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGGCCCCG	CAGGCTGGCA	CTGAGCCGTG	CCCTCCAGAA	GCAGCCGCGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCCGTGAACC	TCGGCAGGGT	AAGGGACGGA	CCTCAGTGGA	1620
GAGATGGCAT	AATTGTCCTG	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCGGA	1680
AAAAGTCAAC	CACCATCCGA	TTCACTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCATCAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTTGCCCT	GCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCTTAAGT	GGCAGGGCGG	GATTACAGC	TGCTTACAGC	GAGAAAGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGGAGAAAT	AAAAGTCCCC	TCCTGGCGTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAGG	2040
TCTGTCAGCT	GGTGTACAAG	GATGGGTCCC	CTTGTCCTTC	CAAATCCGGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCGTG	TGCAGGCTTG	AGGCCGGGCC	AACCAATAGG	CCCAGTCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACTCTCT	TCTTCTCTCT	GCACACGCCG	CTGGCCTGCG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCTTTA	2280
TTCATCGCAC	TGTTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCTGATTTT	CTACATCAAT	ATTGTGACGC	CACTAAATCC	CATGCACGGA	GTGGCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCCTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TTACTTGAAT	TTTGAAAGCA	2520

GTACTCCTTG	CCAGGAATTC	AGTTGTAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAGCTTG	TAATTTTATG	GGACTGCAAA	CAAGGCTTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACTTCTTA	TGTTCTTAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCTGTA	CGACCCAGTA	TCTCTGTCT	TAAGCGTTT	AGTCCCTCAA	CTTCATCTTC	2880
TCCTGGGTTA	AGTTACCCAC	CAGGTAGTTT	GAAGAAAGTT	GTTCCAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCT	TCTACAGTCC	TCCTCATTC	3000
AATTTTATCA	AATTTCTCC	TCATGCGCTG	AAATCTGGCT	GCAACAGAGC	TGCTCTTCTC	3060
GTAGAGGGGC	TCTTTGTAC	CAAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGGC	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTG	CCGAAGTGG	TGACCCCGCG	3180
GGCCAGCCG	GTCTGCGAGC	GATTGGGCGG	TACCACAGAC	ATGCTGGCGA	GCTCCGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGGCGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGAATGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGTGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTTGGAG	TGATGAGAA	GTTTTGGAGC	TAGATAGAAG	TGGTGGTTGT	ACACCATTTG	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAAAACAAG	GATAACATTC	CAACTCTGG	ACATTATCCT	TCCTTTCCAT	TTGATGTCAG	360
GCCCGTGTTA	GAATTCTCAT	CCGGTTTGGT	CACTGCACCT	AAGATGTGGA	GAAATTAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTTCTAGG	TTTCCCTTAA	480
ACAATTTAAC	AGATGGATAG	TGGCACCAC	TACGAGATGG	AAAAACCAGC	GGAAGGAAGA	540
TTTGGGGGAG	AAGTTAAGTT	TGTCTTGGGC	CTGTGTTTTG	CAACCTGAGT	GTAAAAAGACA	600
TATGTTAAGT	CTTCAGTGGC	GAAACACTAA	AACTAGAAAT	GGATCAGAAT	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GTCTTGTCTC	TTCAAGTGCCT	GGTCAAAATG	CAAGATGGGC	720
AATCTTTTCC	TGAAGGTCCA	AGCACCTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTGCT	780
TAGAACAAATC	CTAGTTTCTG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTTTGT	GCAATAAATT	CTGCAACGTG	ATGGCCGCGC	TCTCGCGGCC	CGAGCGGCCG	900
GACCTTGTCT	TGAGGAAGA	GGACCTCCCC	TATGAGGAGG	AAATCATGCG	GAACCAATTC	960
TCTGTCAAAAT	GCTGGCTTCA	CTACATCGAG	TTCAAACAGG	CGCCCCGAA	GCCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGTG	TGACCCGACC	TGCCTATGAA	1140
GATGTCAACA	ACTGTCTATG	GAGGGCCTTT	GTGTTTATGC	ACAAGATGCC	TCGTCTGTGG	1200
CTAGATTACT	GCCAGTTTCT	CATGGACGAG	GGGCGCGTCA	CACACACCCG	CCGCACCTTC	1260
GACCGTGCCC	TCCGGGCACT	GCCCATCACG	CAGCACTCTC	GAATTTGGCC	CCTGTATCTG	1320
CGCTTCTGTC	GCTCACACCC	ACTGCCTGAG	ACAGCTGTGC	GAGGCTATCG	GCGCTTCTCT	1380
AAGCTGAGTG	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCCGCTG	1440
GATGAGGCCG	CCCAGCGCCT	GGCCACCGTG	GTGAACGACG	AGCGTTTCGT	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGCT	GTGGCACGAG	CTGTGCGACC	TCATCTCCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCGCGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGGCA	AGCTCTGGTG	TTCTCTCGCC	GACTACTACA	TCCGCAGCGG	CCATTTCTGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGCG	GGACTTCACA	1740
CAGGTGTTTG	ACAGTACTCG	CCAGTTCTGAG	GAGAGCATGA	TCGCTGCAAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGAGGAGGAT	GATGTGGACC	TGGAGCTGCG	CCTGGCCCGC	1860
TTCGAGCAGC	TCATCAGCCG	GCGGCCCTTG	CTCCTCAACA	GCGTCTTGCT	GCGCCAAAC	1920
CCACACCACG	TGCACGAGTG	GCACAAGCGT	GTCGCCCTGC	ACCAGGGCCG	CCCCCGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCAG	ACGGTGGACC	CCTTCAAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	GTTTGCCAAG	TTTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCCGTGTA	TCTGTGAGAA	GGCCACCAAG	GTGAACTTCA	AGCAGGTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTGAGTGGG	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCCTTG	2220
CGGCTGCTGC	GAAAGGCCAC	GGCGCTGCCT	GCCCGCCGGG	CCGAGTACTT	TGATGGTTCA	2280
GAGCCCGTGC	AGAACCAGCT	GTACAAGTCA	CTGAAGGTCT	GGTCCATGCT	GCGCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAGGCCGTGT	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCCTGGAGGA	GCACAAGTAC	2460
TTGAGGAGAG	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAAA	TTTATTGCCC	GCTATGGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	GCCCCCAAA	ATATGCCAAG	2640
ACCTTGTACC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
GCCGTGTACG	AGCGTGCCAC	CAGGCGCGTG	GAGCCCGCCC	AGCAGTATGA	CATGTTCAAC	2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCAG	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCCTGCG	GTTTGACAGC	2880
ATGGAGTGCA	AGCTCGGGGA	GATTGACCGC	GCCCGGGCCA	TCTACAGCTT	CTGCTCCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGCGCGTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAAATT	CATGGCCTCG	CAGATGCTCA	AGGTCTCGGG	CAGTGCCACG	3120
GGCACCCTGT	CTGACCTGGC	CCCTGGGCGAG	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCGGGCAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCTTGCG	CGCCACAGGC	3240
AAGATCCTGT	TCGTGAGGAG	TGACGCTCC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTGGGCTGGA	GCAGCAGAGC	GTGCCAGCCG	CAGTGTGTTG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCCCTC	GTGCCGAATT	CGGCACGAGC	AAGACCAAGC	CCCAGATCAT	3480
TTGCCTCAAA	GGTTTTCCCT	CGAAGTCACA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTTTGAAGTG	TGGGCATTGG	TGGCCTGTGG	CTGTGCTCTC	TCTCTGTAGC	TGTTTICTCC	3600
CTACATCCCT	GAAAGGAAGT	TGAGCCTGCT	CCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGCTCC	TGGCCTCCAG	3720
GCCCGTGTCC	CTCTGTCTC	TAGCCCACTA	AGGCCCTGGC	CCATTGTGTC	TAAACAGGCA	3780
GTCCGACCTA	GAAAGAGCAG	ACAATCTCTC	TGGGTCAACA	GTCTGGCTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCCT	TCTCCCCTGC	CCATGTGAAT	TCCCAGGGGC	AGAGCCTGAA	3900
ATGTTGAACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCCT	3960
CCTGCCTGCT	TTCTGTTGTT	CAGAGTAGCT	GAGGCTTGTG	TGAGAGGAGT	TGGAGTGCTG	4020
GTTTTACCCC	TGGTTGGTGT	GCTTTGCTTT	GAGGGCAGTT	AGAAAGCCCA	GCCCAGCCCT	4080
TGCTCTGCC	CTGCACACAG	CGGAGCGACT	TTTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GCAGCAGGTG	GCATGGAGCC	AAGAGGAAAT	GTGACTGAAA	CTGTCCACTC	ATAGCCCGGC	4200
TGCCGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGCGC	GCCTGCAGGT	CGACACTAGT	GGATCCAAAG	AATTCGGCAC	GAGGGAAACT	60
CAACGGTGTA	CGAGTGGAGG	ACAGGGACAG	AGCCCTCTGT	GGTGGAACGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAGTGTCTGA	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGGCA	240
TCTTCCCGGA	ATCAGATTCA	AAGGATCCTG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTTT	CGAGATCACA	GTGCTGGAAG	CAGGAACCCA	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCCA	TGCCCTGACA	CTGCTGAAT	ACACTGAGAC	CCGGAATCAG	TTCTTTGATG	420
AGCTCATGGA	GCTTGAGATC	TTCTTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCCAGCTGG	CTCCAGCCAT	CCTGCAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGCTGG	AGGATCTGAT	TGGCAAGCTT	ACCACTCTTC	600
AGCTGCAACA	CCTGTTTATG	ATCCTGGCCT	CACCAAGGTA	TGTGGACCGA	GTGACTGAAT	660
TCCTCCAGCA	AAAGCTGAAG	CAGTCCCAGC	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAAGCAGCA	GGAGGCACCT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAAGCTGA	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACCTGATG	GGAACCTCTC	TGTGACACCC	TCCGTGTTCT	TGCCTGCCCA	900
TCTTCTCCGC	TTTTGGGATG	AAGATGATAG	CCAGGGCTGT	TGTTTTGGGG	CCCTTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GCCACAGGAA	GGAAGCGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAGA	AGCTGTGGTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTTCT	CGAGAGTACT	1140
TCTAGAGCGG	CCGCGGGCCC	ATCGATTTC	CACCCGGGTG	GGGTACC		1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGGAACAAA	AGCTGGAGCT	CGCGCGCCTG	CAGGTGACCA	CTAGTGGATC	60
GAAAGTTCGT	TACGCCAAGC	TCGAAATTAA	CTCTGGGCTG	ACCCATAAAC	ATTGTCTGTA	120

TCTAGGATAT AGTTGCGTTT CTTGCGGGCA GCAATCTGGA TGAGGCGGTT GAGGCACTGG 180
GTGGCCTGCT GGATCAGGAC ATCCCAGCGG CCAGCATAGT TCCGCTGCCG GCGTAGGCCC 240
ATCACCCGCA TCTTATCCAT GATGGCATTG GTACCCAGGA TGTGTACTT CTTGGAAGGG 300
TTGGAGGCTG CATGTTTGAT GGCCCATGTG GTCTTGCCAG CAGCAGGCAG GCCCACCATC 360
ATCAGAATCT CACATTCTGC CTTGCTCTTT GGTCCAACGG TGCCCCGGAT ACGCTCACTA 420
AGGGGAAGGT GCTGGATGAA GGTAAACCCC GGGAGGACAG AACAGTAGGG CTCTGCTCTC 480
TGTCCGAAGT TGAACCTCCAC TGCCTCAATC TTCACCAGGA CATGAGGATA GAGGGCCTGA 540
CCCCCAAGG CTTCTTCTG GATTGCGAAA GCAATGCCCA TCCACTTTCC ATTCTTGGA 600
AAAGACAGTT CCACGTCATT TCCACATTCA AAATCCGCAA AGCAGCCAAT CACCGGAGAG 660
CTCTGCGGTG CTAGGAGAGC GGCTGGGCCC GCAGACTGGG GGGAAAGCTC CGCAGCCGCA 720
GTGGGCCCCA GGATCAGGCC CCGCTGGGCC TGGAGAAACC CAGTCTGGGC TGGAGCGGGA 780
GCTGGACAGT GTGGCCTTGC GTTCCGCCCC GGGAGCGCTG CGAGTGTGCG GGCCTCGGGT 840
GGATTTGCTG AGCACCATAA CCTCACGTTT GCCAACCTGG GGTTTTAGCT CCCTTGTTT 900
TAATCCCTA GGGCGGGTG GGGGCACGGG AGGAAGGATG GGCAGCTGG GTGCAATCCT 960
GCTGTAAGCC AGCCATTCTT TGATTTCTTA GAATTAATA AACGGTCGCG CCGGAGGCCG 1020
CGGGGGCCGG AGCGGAGCAG CCGCGGCTGA GGTTCGCGAG TCGGCCGCTC GGGGCTGCGC 1080
TCCGCCGCGG GAGCCCCGGC CTCTGGCCGC GCCGCTCCG GCCTCCGGGG GGGCCGGGCG 1140
CGCCGGGACA TGGTGCCAGT CGCACCCCTT CCCCGCCGCC GCTGAGCTCG CCGGCCGCGC 1200
CCGGGCTGGG ACGTCCGAGC GGAAGATGT TTTCCGCCCT GAAGAAGCTG GTGGGTCGG 1260
ACCAGGCCCC GGGCCGGGAC AAGAACATCC CCGCCGGGCT GCAGTCCATG AACGAGCGT 1320
TGCAGAGGCG CTTGCGCAAG GGGGTGCAGT ACAACATGAA GATAGTGATC CGGGGAGACA 1380
GGAACACGGG CAAGACAGCG CTGTGGCACC GCCTGCAGGG CCGGCCGTTT GTGGAGGAT 1440
ACATCCCCAC ACAGGAGATC CAGGTCACCA GCATCCACTG GAGCTACAAG ACCACGGATG 1500
ACATCGTGAA GGTGAAAGTC TGGGATGAG TAGACAAAGG AAAATGCAA AAGCGAGGCG 1560
ACGGCTTAAA GATGGAGAAC GACCCCAAGG AGNCGGAGTC TGAATGGCC CTGGATGCTG 1620
AGTTCCCTGA CGTGACAAAG AACTGCAACG GGGTGGTCAT GATGTTGAC ATTACCAAGC 1680
AGTGGACCTT CAATTACATT CTCCGGAGC TTCCAAAAGT GCCCACCCAC GTGCCAGTGT 1740
GCGTGCTGGG GAACATCCGG GACATGGGCG AGCACCGAGT CATCTGCCG GACGACGTGC 1800
GTGACTTCAT CGACAACCTG GACAGACCTC CAGGTTCCCT CTACTCCGC TATGCTGAGT 1860
CTTCCATGAA GAACAGCTTC GGCCTAAAGT ACCTTCATAA GTTCTTCAAT ATCCCATTTT 1920
TGCAAGTTCA GAGGGAGACG CTGTTGCGGC AGCTGGAGAC GAACCAGCTG GACATGGACG 1980
CCACGCTGGA GGAGCTGTCG GTGCAGCAGG AGACGGAGGA CCAGAACTAC GGCATCTTCC 2040
TGGAGATGAT GGAGGCTCGC AGCCGTGGCC ATGCGTCCCC ACTGGCGGCC AACGGGCGA 2100
GCCATCCCC GGGCTCCCAG TCACCAATCC TGCTTGACCC CGCTGTGTCC ACGGGGAGCT 2160
CCAGCCCCGG CACACCCAG CCGCCCCAC AGCTGCCCT CAATGTGTCC CCACCATCCT 2220
CTGTGCCCCC TGACCAACC TCAGAGGCCG TGCCCCCACC TGCGTGCCCC TCAGCCCCCG 2280
CCCCACGGCG CAGCATATC TCTAGGCTGT TTGGGACGTC ACCTGCCACC GAGGCAGCCC 2340
CTCCACCTCC AGAGCCAGTC CCGGCCGAC AGGGCCGAGC AACGGTCCAG AGTGTGGAGG 2400
ACTTTGTTCC TGACGACCGC CTGGACCGCA GCTTCCTGGA AGACACAACC CCGCCAGGG 2460
ACGAGAAGAA GGTGGGGGCC AAGGCTGCCC AGCAGGACAG TGACAGTAT GGGGAGGCC 2520
TGGGGGCGAA CCCGATGGTG GCAGGGTTCC AGGACGATG GGACCTCGAA GACCAGCCAC 2580
GTGGGAGTCC CCGCTGCCT GCAGGCCCCG TCCCCAGTCA AGACATCACT CTTTCGAGTG 2640
AGGAGGAAGC AGAAGTGGCA GCTCCCAAA AAGGCCCTGC CCCAGTCCC CAGCAGTGT 2700
CAGAGCCAGA GACCAAGTGG TCCTCCATAC CAGCTTCGAA GCCACGGAGG GGGACAGCTC 2760
CCACGAGGAC CGCAGCACCC CCCTGGCCAG GCGGTGTCTC TGTCGCACA GGTCCGAGA 2820
AGCGCAGCAG CACCAGGCC CCGCTGAGA TGGAGCCGGG GAAGGGTGAG CAGGCCTCTC 2880
CGTCGGAGAG TGACCCCGAG GGACCCATTG CTGCACAAAT GCTGTCTTC GTCATGGATG 2940
ACCCGACTT TGAGAGCGAG GGATCAGACA CACAGCGCAG GCGGATGAC TTTCCCGTGC 3000
GAGATGACCC CTCCGATGTG ACTGACGAGG ATGAGGGCCC TGCCGAGCCG CCCCCACCCC 3060
CCAAGCTCCC TCTCCCCGCC TTCAGACTGA AGAATGACTC GGACCTCTTC GGGCTGGGGC 3120
TGGAGGAGGC CGGACCCAAG GAGAGCAGTG AGGAAGGTAA GGAGGGGCAA ACCCCCTCTA 3180
AGGAGAAGAA AAAAAAACA AAAAGCTTCT CGAGAGTACT TCTAGAGCGG CCGCGGGCCC 3240
ATCGATTTC CACCCGGGTG GGTACCAGG TAAGTGATCC CAATTCGCC TATAGTGAGT 3300
CGTATT

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTTCCGT CTCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTC AGAAATTCAG

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCAGTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCACAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
GGTTGGAGAA CTGGATGTAG 20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
CTATTCAGAT GCAACGCCAG 20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
CCATGGCACA CAGAGCAGAC 20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
GCTACCATGC AGAGACACAG 20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
CAGGCTGACA AGAAAATCAG 20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
GGCAGCATA GAGGAGAGAC 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCCTCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTT CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCAACC TGAGGCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAGTG

20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTGC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GCGGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCAGGA AGCTGCCGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCAACAGTG GTGCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCGTC CGGGAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 378...1799
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTTCC CGGGCCCGCG GCGATGCCCC    60
CCCGGTAGCT CGGGCCCGTG GTCGGGTGTT TGTGAGTGT TCTATGTGG AGAAGGAGGA    120
GGAGGAGGAA GAAGAAGCAA CGATTTGTCT TCTCGGCTGG TCTCCCCCG GCTCTACATG    180
TTCCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCTCCCG GCCCGGATTA    240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CCTTGGATT AGACGCCGAT TCGCCAGTG    300
TTTGGGAAAT GGGAAAGTAA GACAGCTGGC ACCTGAACTA AGTACTTTTA TAGGCAACAC    360
CATTCCAGAA ATTCAAG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT    410
                Met Asn Gly Asp Met Pro His Val Pro Ile Thr
                1                5                10

ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT    458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro
                15                20                25

CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT    506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn
                30                35                40

GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC    554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp
                45                50                55

AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT    602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp
                60                65                70                75

CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC    650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp
                80                85                90

ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC    698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe
                95                100                105

AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG    746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met
                110                115                120

TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT    794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser
                125                130                135

TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT    842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe
                140                145                150                155

GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT    890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn
                160                165                170

AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG    938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met
                175                180                185

CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA    986
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln
                190                195                200
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GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC CAGTTGGCTT CTCTCACTCG CTTCTCCTG TGGAGAAGCC TGTCCAGGTG TCACTGCCTC CAGGAAGCTG TCTCTGATTT CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT CGCTCTGTGC CCTGGAATTG TAACCATAGG TTTTCTGTG TCCTGGAGGA CAAGGATGAG	1864 1924 1984 2044 2104

GGCTTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT 2164
CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCTT GGCTGCCTGT GTGTTCCAAG 2224
CTAGGAAGAT GTAATGTCCC CACAAACGGG GTAAATGGCT TGCCTGCGTC ACAGCTGTCT 2284
CAAGCCCGAG CCCTGGGGCG CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCGC 2344
CAGGCCACAT CCGCCTCACC TGGGACCCTT TGTGGGTAC AGTCTCCGGC CCCACCCAGA 2404
CCTCCTGAAG GAGAGACCCC ATGGCAAGGA CTCAGCCACC TGCAGTTTCA TAAGCCCCCA 2464
GTGGGTTCCT AGGCATGAAG ACCACCAGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA 2524
GCCCCCTCTC ACCCCAGCCG GGGCCTGCCT CAGAGGCAGC ACCCAGGACG TGGCCATGAC 2584
CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTGAG CCAGCCAGGC 2644
CCCTGGAAGG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCTGCG AACTGCCAGG 2704
TGCAGCACAC GACCCGTGTC CCGTGTTCGA TAGCAGGGAG CCATGACCTG GCAACGATTG 2764
CAGGCTCAAA GGGGCACCCG GGGGGCCCTG GGTGGGGCG GATCAGCTTT CCCTGGGCAC 2824
ATCTGCCTCA TTCCAGATCT CCAGGGCTCA TGTCTGTGAC AGGGAGGGAA GGCTCTGCCC 2884
TGGCCTTCGG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTTAGA GCTGGCTTCT 2944
GCCCACACTT TCTCCGTGAA AGGAAAACAA CTATGAGTCT GCCAAACGCA TCTCAGATGC 3004
GTTTAAAAA ATTCTGGTCC CCGCTCTCTG TCCCATCATC CGCCTCGGGG ACTTCCTCTC 3064
TCCGTGGTTC TCACCCCATATA CTCTGTCACT GCCACATTTT CACCTGGGCC TGGCCTTTGT 3124
CTCCACCTGA AACTCCTGAA AATCTTGAAG TGGATTTCTA GGTCACTGGG GACTCCGGCA 3184
GCACATTCGG CTTCAGAATA AAGGGCGCCC GCGGTCCCCC AGCACCTCCC CAAGCCACAC 3244
CCCTAGCTTC CCTCCCTATC CCTGCAGCCT GAGGGTCCCT TCAGCCACCC TTAAGTCCCC 3304
ACCTGGGCTC CTGCCCGGCC CCTGGCTAGC AGCGCCTTCT CCACCGGGGC CCCCTCTGCT 3364
CACAGAGCCC CCTCACCTCC CTGGGGATGA GGGGCCAGGC CATGACCCTG AAAGTCTAGC 3424
CCTGGCCTTG ACCTCCAGG AGCGCCCTCC CCGCCCTCTC CCGGCCCGG CCCCGTCTC 3484
TGCTGTGGC CTCTGGGTG TGGCCCGCAG ACTGAGCTGC GCTTGGGGGT CCTGGCGGCC 3544
TGGGCGGTCC CGCACCGAAC CCAGGCGGTC GGAGCCCGGC GGGAGGGCGG GAGGTCTTTC 3604
TGGGGGTCC TCCGACGCT GAGGGCGCTG CTTCGCCGCG GCCGCCCGG GTTCTGCGG 3664
AGCCGGGGCC TCCGCTCTCG GGTGACCCGG TGAGACCCCC GGGGAGGCGG CTGGGGAGGC 3724
GCGGGCTCTG CTCCCGGTC CCAAACGCAC TGGCTGCCCC TCAGGAGGGA CGGCGACCTC 3784
CACCCACGGC GCTGGCGCCC GCACGGCGCG TCCTCCCGCT CCCGACGCCT GGACGCCTCC 3844
CGAGGCGGCC CCGCCGGGCC CCACGCGCGG CCCCATCCGC AGGCCAGGAC TGCCTTCCCG 3904
GAGCTGGCGG CCCCAGCCT GGAGGAGCGG GCCCCAGAG CCCTCCAGC CCTCCCCAGC 3964
CCACTCTGGC CCGCAGCCG CCGCCTGGTC CGAGTGGGG TCTCTGGCCC CGGCCTTTCC 4024
CGGGGAAGGA AAGCAAAAG CTT 4047

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear.

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
1 5 10 15
Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
20 25 30
Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
35 40 45
Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
50 55 60
Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
65 70 75 80
Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
85 90 95
Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
100 105 110
Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met Ser Gln Tyr Lys Leu
115 120 125
Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
130 135 140
Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
145 150 155 160
Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
165 170 175
Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
180 185 190
Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
195 200 205

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235 240
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2998 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 26...799
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTGG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly Leu Gln Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val
75 80 85

GAG TTG CTT TTG AAA TCA GAA AGT CAG TGC AGG GTT GTA GTG TTG ATG 340
Glu Leu Leu Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met 105
90 95 100

GGC TCT ACT TCT GAT CTT GGT CAC TGT GAA AAA ATC AAG AAG GCC TGT 388
Gly Ser Thr Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys 120
110 115

GGA AAT TTT GGC ATT CCA TGT GAA CTT CGA GTA ACA TCT GCG CAT AAA 436
Gly Asn Phe Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys 135
125 130

GGA CCA GAT GAA ACT CTG AGG ATT AAA GCT GAG TAT GAA GGG GAT GGC 484
Gly Pro Asp Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly 150
140 145

ATT CCT ACT GTA TTT GTG GCA GTG GCA GGC AGA AGT AAT GGT TTG GGA 532
Ile Pro Thr Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly 165
155 160

CCA GTG ATG TCT GGG AAC ACT GCA TAT CCA GTT ATC AGC TGT CCT CCC 580
Pro Val Met Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro 185
170 175 180

CTC ACA CCA GAC TGG GGA GTT CAG GAT GTG TGG TCT TCT CTT CGA CTA 628
Leu Thr Pro Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu 200
190 195

CCC AGT GGT CTT GGC TGT TCA ACC GTA CTT TCT CCA GAA GGA TCA GCT 676
Pro Ser Gly Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala 215
205 210

CAA TTT GCT GCT CAG ATA TTT GGG TTA AGC AAC CAT TTG GTA TGG AGC 724
Gln Phe Ala Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser 230
220 225

AAA CTG CGA GCA AGC ATT TTG AAC ACA TGG ATT TCC TTG AAG CAG GCT 772
Lys Leu Arg Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala 245
235 240

GAC AAG AAA ATC AGA GAA TGT AAT TTA TAAGAAAGAA TGCCATTGAA TTTTTTA 826
Asp Lys Lys Ile Arg Glu Cys Asn Leu 255
250

GGGGAAAAAC TACAAATTTT TAATTTAGCT GAAGGAAAAAT CAAGCAAGAT GAAAAGGTAA 886
TTTTAAATTA GAGAACACAA ATAAATGTA TTAGTGAATA AATGGTGAGG GTAGGCCTAT 946
TCAGATGCAA GGCCAGCAAT GGGGCTCCCC ATTATCCCCA CCCCTTTGGT CCCAGTCCCC 1006
TTCTCTGCAA TGGGCACGCA TAGAGGAGAG ACAAAGGGA TTAGACGCAA CATCATTTGGC 1066
CCAGGGGAGT CCGAGAAGAG CTGCCATTGG CTGACAGGGC ATTTTCAGGC TCTGTCTATTG 1126
GTCAGGGAGC ACACCCAGC CTGAAGAGTG ATGCCATTGG CCAGGGAGTG GTTTTGTCTAT 1186
AGCCGTTGGC TGTGAAGTGG AAGGAAAAGA TCTGGGAATG AAGCCCTGTG GCCAGGAAGA 1246
TAGACAGGGC AGCAACTTCT GGGCCTCCAG GCCCTCTTCC CACCATAGCA ATGTGGGCAA 1306
AACTGGTGTC AGGCCCCAGC CAGAAAAAGG AGCCCAAGCC AGAGGGCAAG TGACAAAGGA 1366
TGTACCATGT CCAATCTCCC ACACCCTGGG GCTGCCCTTC CCAATGTCTT TCTTGATAGC 1426
CAAGTTGGGC TGGGAGCAGC TCACTGCTCC TCTAGCCAGG AGGGTTTCTC AGCTCCTGGA 1486
GGCCGCAGCT TGATGTTGAA CTGCTGCAGG GTCTGCTCCA GCTGTTTCTG GTTCCCAGCA 1546
AAGTAGGCGG ACACAGCATT GTGGAAGAGC AGCAGCTGCT TGTGCATCAC CTTGATCTTG 1606
TTTTCTTCCA GGAACCTTGA CTGATGGGCC ACATCTCCCC GCAGCTTCTC ATACTTGTCC 1666
CGATGGGCCT GGAAAGTGGC CTGGGCACTC TCAAGTCGAC CACGTGTCCC TGACATCCCCG 1726
GGGCCCTAGC TCAGCTCCTC TAAGTCTGTT CGGTAGGCAT CATATTCCAG CCTGGCAGCC 1786
TCATACTGTT TCACAGTCAT GAGCGTGTCT TCCATGGTCT TGGTGACCAA TGTGTTGATG 1846
CTAGAGACAA AGAAGTTCAC GGCTCCTAGC AGCGTTTCCC CATTCTTGCA TAGTAGTTTC 1906
TGTGTCTCTG CATTGTAGCC AAATTCCTCC TGAAGCTCTG GGGACTTCTG GCTGAGGTCA 1966
GCAAAGGCAT CACCCAGTGC ATGCTGGGTC TGCAGCAGGC TGTAGAGGTG GGCTGTCACT 2026
GCCCGGCCCA GCTGCAGGAC ACTCTCATAC TTGCGTTTCG TCTCACGCAG CAACTCAATC 2086
TGCAGCTCTA GCTCCAGGAT TCCGGCGCCT CCACTCCGTC CCCCAGGGT CTGCTCTGTG 2146
TGCCATGGAC GGCATTGTCC CAGATATAGC CGTTGGTACA AAGCGGGGAT CTGACGAGCT 2206
TTTCTCTACT TGTGTACTA ACGGACCGTT TATCATGAGC AGCAACTCGG CTTCTGCAGC 2266
AAACGGAAAT GACAGCAAGA AGTTCAAAGG TGACAGCCGA AGTGCAGGCG TCCCCTCTAG 2326
AGTGATCCAC ATCCGGAAGC TCCCCATCGA CGTCACGGAG GGGGAAGTCA TCTCCCTGGG 2386

GCTGCCCTTT GGAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCCTTCAT 2446
CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC 2506
TGTGCTGCGC GGCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA 2566
CAGCTCTCCC AACCAGGCGC GGGCCAGGC GGCCTGCAG GCGGTGAAC TCGTCCAGTC 2626
GGGGAACCTG GCCTTGGCTG CCTCGGCGC GGCCTGGAT GCAGGGATGG CGATGGCCGG 2686
GCAGAGCCCC GTGCTCAGGA TCATCGTGA GAACCTCTTC TACCCTGTGA CCTGGATGT 2746
GCTGCACCAG ATTTTCTCCA AGTTCGGCAC AGTGTGAAG ATCATCACCT TCACCAAGAA 2806
CAACCACTTC CAGGCCCTGC TGCAGTATGC GGACCCCGTG AGCGCCAGC ACGCCAAGCT 2866
GTCGCTGGAC GGGCAGAACA TCTACAACGC CTGCTGCACG CTGCGCATCG ACTTTTCCAA 2926
GCTCACCAGC TCACACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA 2986
TTCTTTGGAT CC 2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln
1 5 10 15
Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
20 25 30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
35 40 45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
50 55 60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
65 70 75 80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Lys Ser Glu
85 90 95
Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
100 105 110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
115 120 125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
130 135 140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
145 150 155 160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
165 170 175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
180 185 190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
195 200 205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
210 215 220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
225 230 235 240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
245 250 255
Asn Leu

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
1 5 10 15

Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595 600 605
 Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys
 610 615 620
 Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
 625 630 635 640
 Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
 645 650 655
 Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
 660 665 670
 Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
 675 680 685
 Thr Ile Pro Ala Pro Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
 690 695 700
 Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
 705 710 715 720
 Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
 725 730 735
 Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
 740 745 750
 Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
 755 760 765
 Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
 770 775 780
 Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
 785 790 795 800
 Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
 805 810 815
 Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
 820 825 830
 Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
 835 840 845
 Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
 850 855 860
 Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
 865 870 875 880
 Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
 885 890 895
 Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
 900 905 910
 Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
 915 920 925
 Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
 930 935 940
 Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln
 945 950 955 960
 Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
 965 970 975
 Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
 980 985 990
 Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
 995 1000 1005
 Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
 1010 1015 1020
 Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Lys Gln Lys Ala
 1025 1030 1035

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
 1 5 10 15
 Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
 20 25 30
 Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
 35 40 45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
 50 55 60
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
 65 70 75 80
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
 85 90 95
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
 100 105 110
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
 115 120 125
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
 130 135 140
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
 145 150 155 160
 Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
 165 170 175
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
 180 185 190
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
 195 200 205
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
 210 215 220
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
 225 230 235 240
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
 245 250 255
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
 260 265 270
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
 275 280 285
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
 290 295 300
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
 305 310 315 320
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
 325 330 335
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
 340 345 350
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
 355 360 365
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
 370 375 380
 His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
 385 390 395 400
 Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
 260 265 270
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
 275 280 285
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
 290 295 300
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
 305 310 315 320
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
 325 330 335
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
 340 345 350
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
 355 360 365
 Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
 370 375 380
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
 385 390 395 400
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
 405 410 415
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
 420 425 430
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
 435 440 445
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
 450 455 460
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
 465 470 475 480
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
 485 490 495
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
 500 505 510
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
 515 520 525
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
 530 535 540
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
 545 550 555 560
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
 565 570 575
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
 580 585 590
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
 595 600 605
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
 610 615 620
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
 625 630 635 640
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
 645 650 655
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
 660 665 670
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
 675 680 685
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
 690 695 700
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
 705 710 715 720
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
 725 730 735
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
 740 745 750
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
 755 760 765
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
 770 775 780
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
 785 790 795 800
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile
 805 810 815
 Gln Leu Gly Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
 820 825 830
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835
Leu Lys Glu Asp
850

840

845

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
1 5 10 15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
20 25 30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
35 40 45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
50 55 60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
65 70 75 80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
85 90 95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100 105 110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
115 120 125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130 135 140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145 150 155 160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165 170 175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
180 185 190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
195 200 205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
210 215 220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225 230 235 240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
245 250 255
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
260 265 270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
275 280 285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
290 295 300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305 310 315 320
Pro Gln Leu Pro Lys Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
325 330 335
Pro Pro Ser Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala
340 345 350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
355 360 365
Glu Ala Ala Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
370 375 380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
385 390 395 400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
405 410 415
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
420 425 430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
435 440 445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
450 455 460

Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
 465 470 475 480
 Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
 485 490 495
 Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
 500 505 510
 Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
 515 520 525
 Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
 530 535 540
 Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
 545 550 555 560
 Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
 565 570 575
 Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
 580 585 590
 Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
 595 600 605
 Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
 610 615 620
 Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser
 625 630 635 640
 Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
 645 650 655
 Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
 660 665 670
 Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
 675 680 685
 Tyr Ser Glu Ser Tyr
 690